

FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'
ENTERED AT 12:13:03 ON 12 JAN 2006

L1 42112 S TRANSMEMBRANE (W) (PROTEIN? OR POLYPEPTIDE?)
L2 83 S CYSTATIN(W)LIKE(W)DOMAIN
L3 1 S L1 AND L2
L4 1286 S (ALPHA OR A) (W)2(W)HS(W)GLYCOPROTEIN
L5 1 S L1 AND L2 AND L3
L6 1 S L1 AND L3
L7 1 S L2 AND L3
L8 3205318 S (INFLAMMAT? OR (CANCER OR TUMOR) OR PROLIFERAT? OR DIFFERENTI
L9 162 S L4(P)L8
L10 258 S L4(S)L8
L11 94 DUP REM L9 (68 DUPLICATES REMOVED)
L12 29 S 1950-1998/PY AND L11

=>

Refine Search

Search Results -

Terms	Documents
L1 and L2 and L3	1

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

Search History

DATE: Thursday, January 12, 2006 [Printable Copy](#) [Create Case](#)

Set Name Query

side by side

Hit Count Set Name

result set

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR

<u>L5</u>	L1 and L2 and L3	1	<u>L5</u>
<u>L4</u>	L1 same L2 same L3	0	<u>L4</u>
<u>L3</u>	(alpha or a) adj 2 adj glycoprotein	97	<u>L3</u>
<u>L2</u>	cystatin NEAR1 domain	32	<u>L2</u>
<u>L1</u>	transmembrane adj (protein\$1 or polypeptide\$1)	9646	<u>L1</u>

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:14:03 ; Search time 190 Seconds
(without alignments)
883.383 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCCGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2018	100.0	382	2	AAW88491	Aaw88491 Human liv
2	2018	100.0	382	3	AAB25782	Aab25782 Human sec
3	2018	100.0	382	4	AAB75368	Aab75368 Human sec
4	2018	100.0	382	8	ADP19169	Adp19169 Human sec
5	2015	99.9	382	4	AAB51346	Aab51346 Human HS-
6	2010	99.6	382	8	ADJ75395	Adj75395 Marker ge
7	2001	99.2	382	7	ADE40170	Ade40170 Human NOV
8	1925.5	95.4	369	7	ADE40172	Ade40172 Human NOV

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:18:29 ; Search time 48 Seconds
(without alignments)
657.961 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCGGAMS.....ARTAECPGPAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2018	100.0	382	2	US-09-599-360B-93
2	1632	80.9	314	2	US-09-949-016-11341
3	421	20.9	81	2	US-09-513-999C-7797
4	274	13.6	367	1	US-08-737-045-14
5	274	13.6	367	2	US-08-932-871B-2
6	274	13.6	367	2	US-09-476-919-2
7	274	13.6	367	2	US-08-780-311A-2
8	265.5	13.2	364	1	US-08-483-926A-10
9	265.5	13.2	364	1	US-08-737-045-10
10	254	12.6	349	1	US-08-483-926A-12
11	253.5	12.6	361	1	US-08-483-926A-9

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:26:49 ; Search time 163 Seconds
(without alignments)
979.207 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCGGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2018	100.0	382	3	US-09-978-360A-425	Sequence 425, App	
2	2018	100.0	382	4	US-10-315-664-93	Sequence 93, Appl	
3	2018	100.0	382	5	US-10-626-686-1	Sequence 1, Appli	
4	2010	99.6	382	5	US-10-631-467-647	Sequence 647, App	
5	2001	99.2	382	4	US-10-210-172-76	Sequence 76, Appl	
6	1925.5	95.4	369	4	US-10-210-172-78	Sequence 78, Appl	
7	1925.5	95.4	369	4	US-10-210-172-80	Sequence 80, Appl	
8	1833	90.8	356	4	US-10-210-172-84	Sequence 84, Appl	
9	1787.5	88.6	345	4	US-10-210-172-86	Sequence 86, Appl	
10	1612.5	79.9	317	4	US-10-210-172-82	Sequence 82, Appl	
11	274	13.6	367	5	US-10-626-686-57	Sequence 57, Appl	

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:26:00 ; Search time 12 Seconds
(without alignments)
214.454 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCCGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	274	13.6	367	6	US-10-888-962-6	Sequence 6, Appli
2	245.5	12.2	352	6	US-10-888-962-8	Sequence 8, Appli
3	242	12.0	345	6	US-10-888-962-7	Sequence 7, Appli
4	242	12.0	359	6	US-10-888-962-5	Sequence 5, Appli
5	110	5.5	1005	7	US-11-113-424-63	Sequence 63, Appl
6	99	4.9	448	6	US-10-967-527A-16	Sequence 16, Appl
7	96.5	4.8	1142	7	US-11-044-051-73	Sequence 73, Appl
8	95	4.7	437	6	US-10-995-561-931	Sequence 931, App
9	95	4.7	447	6	US-10-995-561-930	Sequence 930, App

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:18:49 ; Search time 573 Seconds
(without alignments)
921.303 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCGGAMS.....ARTAECPGPAQNASPLVLP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
- 15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
- 16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
- 17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
- 18: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
- 19: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
- 20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
- 21: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
- 22: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
- 23: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
- 24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
- 25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
- 26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
- 27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:*

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:22:10 ; Search time 14 Seconds
(without alignments)
262.433 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCCGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57320 seqs, 9617956 residues

Total number of hits satisfying chosen parameters: 57320

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Length	DB	ID	Description
		Match				
1	274	13.6	367	7	US-11-268-554-157	Sequence 157, App
2	274	13.6	367	7	US-11-268-554-158	Sequence 158, App
3	267.5	13.3	366	7	US-11-268-554-159	Sequence 159, App
4	188.5	9.3	204	7	US-11-268-554-156	Sequence 156, App
5	103	5.1	1015	1	PCT-US05-38668-14	Sequence 14, Appl
6	103	5.1	1015	1	PCT-US05-28839A-82	Sequence 82, Appl
7	103	5.1	1015	7	US-11-259-133-14	Sequence 14, Appl
8	103	5.1	1015	7	US-11-203-251A-82	Sequence 82, Appl
9	103	5.1	1037	1	PCT-US05-38668-12	Sequence 12, Appl

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:15:33 ; Search time 39 Seconds
(without alignments)
942.431 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCGGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	274	13.6	367	1	WOHU	alpha-2-HS-glycopr
2	265.5	13.2	364	2	S22394	fetuin precursor -
3	257.5	12.8	362	2	S22395	fetuin precursor -
4	245	12.1	375	2	A32827	fetuin precursor -
5	242	12.0	345	2	S21094	alpha-2-HS-glycopr
6	242	12.0	359	2	A35714	fetuin precursor -
7	236.5	11.7	348	2	JC5431	countertrypin prec
8	224	11.1	525	1	KGHUGH	histidine-rich gly
9	211	10.5	445	2	A60488	histidine-rich gly
10	204.5	10.1	434	1	KGBOL2	kininogen, LMW II
11	204.5	10.1	436	1	KGBOL1	kininogen, LMW I p
12	204.5	10.1	619	1	KGBOH2	kininogen, HMW II
13	204.5	10.1	621	1	KGBOH1	kininogen, HMW I p

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OM protein - protein search, using sw model

Run on: December 16, 2005, 19:14:43 ; Search time 231 Seconds
(without alignments)
1166.718 Million cell updates/sec

Title: US-10-626-686-1
Perfect score: 2018
Sequence: 1 MGLLLPLALCILVLCGGAMS.....ARTAECPGAQNASPLVLPP 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2018	100.0	382	2	Q6GRB6_HUMAN	Q6grb6	homo sapien
2	2010	99.6	382	1	FETUB_HUMAN	Q9ugm5	homo sapien
3	2005	99.4	382	2	Q6DK58_HUMAN	Q6dk58	homo sapien
4	1783.5	88.4	345	2	Q5J876_HUMAN	Q5j876	homo sapien
5	1608.5	79.7	317	2	Q5J875_HUMAN	Q5j875	homo sapien
6	1318.5	65.3	387	2	Q58D62_BOVIN	Q58d62	bos taurus
7	1263	62.6	388	1	FETUB_MOUSE	Q9qxc1	mus musculu
8	1263	62.6	403	2	Q6YJU2_MOUSE	Q6yju2	mus musculu
9	1259	62.4	388	2	Q8CB17_MOUSE	Q8cb17	mus musculu
10	1207.5	59.8	378	1	FETUB_RAT	Q9qx79	rattus norv
11	1201.5	59.5	393	2	Q6IRS6_RAT	Q6irs6	rattus norv
12	1053.5	52.2	308	2	Q6YJU1_MOUSE	Q6yju1	mus musculu
13	466	23.1	392	2	Q5HZU6_XENTR	Q5hzu6	xenopus tro
14	453.5	22.5	412	2	Q4LDQ0_XENTR	Q4ldq0	xenopus tro
15	436	21.6	415	2	Q6GLH1_XENTR	Q6glh1	xenopus tro